

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.

(ii) TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders

(iii) NUMBER OF SEQUENCES: 58

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

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(B) FILING DATE: 07-SEP-1993
(C) CLASSIFICATION:

(A) APPLICATION NUMBER: US 08/136,783
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(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 396 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTG CTC TGG GTT CCA
Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

48

GGC TCC ACT GGT GAC ATT GTG CTG ACC CAA TCT CCA GCT TCT TTG GCT
Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
20 25 30

96

GTG TCT CTA GGG CAG AGG GCC ACC ATC TCC TGC AAG GCC AGC CAA AGT
Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser

144

35	40	45	
GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAC CAA CAG AAA CCA Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro			192
50	55	60	
GGA CAG CCA CCC AAA CTC CTC ATC TAT GCT GCA TCC AAT CTA GAA TCT Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser			240
65	70	75	80
GGG ATC CCA GCC AGG TTT AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr			288
85	90	95	
CTC AAC ATC CAT CCT GTG GAG GAG GAG GAT GCT GCA ACC TAT TAC TGT Leu Asn Ile His Pro Val Glu Glu Asp Ala Ala Thr Tyr Tyr Cys			336
100	105	110	
CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GGC ACC AAG CTG Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Thr Lys Leu			384
115	120	125	
GAA ATC AAA CGG Glu Ile Lys Arg			396
130			

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Thr	Asp	Thr	Ile	Leu	Leu	Trp	Val	Leu	Leu	Trp	Val	Pro
1				5				10				15		

Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
20 25 30

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
35 40 45

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
50 55 60

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser
65 70 75 80

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

Leu Asn Ile His Pro Val Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
100 105 110

Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Thr Lys Leu
115 120 125

Glu Ile Lys Arg
130

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 64..483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCCGCGG CCGCTATGCA GGGACAATCA GCAGCAGCAA TGAGGAAGTA AGCCTGTGCA	60		
GAT ATG AAC AGC CTT ACT TCC TCA TTG CTG CTG CTG ATT GTC CCT GCA			
Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Leu Ile Val Pro Ala			
1	5	10	15
TAT GTC CTG TCC CAG GTT ACT CTG AAA GAG TCT GGC CCT GGG ATA TTG			
Tyr Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu			
20	25	30	
CAG CCC TCC CAG ACC CTC AGT CTG ACT TGT TCT TTC TCT GGG TTT TCA			
Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser			
35	40	45	
CTG AGC ACT TCT GGT ATG GGT GTG AGC TGG ATT CGT CAG CCT TCA GGA			
Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly			
50	55	60	
AAG GGT CTG GAG TGG CTG GCA CAC ATT TAC TGG GAT GAT GAC AAG CGC			
Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg			
65	70	75	
TAT AAC CCA TCC CTG AAG AGC CGG CTC ACA ATC TCC AAG GAT ACC TCC			
Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser			
80	85	90	95
AGC AAC CAG GTA TTC CTC AAG ATC ACC AGT GTG GAC ACT GCA GAT ACT			
Ser Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr			
100	105	110	
GCC ACA TAC TAC TGT GCT CGA AGA GAG ACT GTG TTC TAC TGG TAC TTC			
Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe			
115	120	125	
GAT GTC TGG GGC GCA GGG ACC ACG GTC ACC GTC TCC TCA			
Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser			

130

135

140

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Ile Val Pro Ala Tyr
1 5 10 15

Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
20 25 30

Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
35 40 45

Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
50 55 60

Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
65 70 75 80

Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser
85 90 95

Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala
100 105 110

Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp
115 120 125

Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
130 135 140

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GTG TTG CAG ACC CAG CAG GTC TTC ATT TCT CTG TTG CTC TGG ATC TCT
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

48

GGT GCC TAC GGG
Gly Ala Tyr Gly
20

60

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser

1

5

10

15

Gly Ala Tyr Gly

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..57

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

48

GTC CAC TCC
Val His Ser

57

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG GTG TTG CAG ACC CAG GTC TTC ATT TCT CTG TTG CTC TGG ATC TCT
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

48

GGT GCC TAC GGG CAG GTT ACC CTG AAA GAG TCT GGC CCT GGG ATA TTG
Gly Ala Tyr Gly Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu
20 25 30

96

CAG CCC TCC CAG ACC CTC AGT CTG ACT TGT TCT TTC TCT GGG TTT TCA
Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser
35 40 45

144

CTG AGC ACT TCT GGT ATG GGT GTG AGC TGG ATT CGT CAG CCT TCA GGA
Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly
50 55 60

192

AAG GGT CTG GAG TGG CTG GCA CAC ATT TAC TGG GAT GAT GAC AAG CGC	240
Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg	
65 70 75 80	
TAT AAC CCA TCC CTG AAG AGC CGG CTC ACA ATC TCC AAG GAT ACC TCC	288
Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser	
85 90 95	
AGC AAC CAG GTA TTC CTC AAG ATC ACC AGT GTG GAC ACT GCA GAT ACT	336
Ser Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr	
100 105 110	
GCC ACA TAC TAC TGT GCT CGA AGA GAG ACT GTG TTC TAC TGG TAC TTC	384
Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe	
115 120 125	
GAT GTC TGG GGC GCA GGG ACC ACG GTC ACC GTC TCC TCA	423
Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser	
130 135 140	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser	
1 5 10 15	
Gly Ala Tyr Gly Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu	
20 25 30	

Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser
35 40 45

Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly
50 55 60

Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg
65 70 75 80

Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
85 90 95

Ser Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr
100 105 110

Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe
115 120 125

Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
130 135 140

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG GTG TTG CAG ACC CAG GTC TTC ATT TCT CTG TTG CTC TGG ATC TCT

48

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser			
1	5	10	15
GGT GCC TAC GGG CAG GTT ACC CTG CGT GAA TCC GGT CCG GCA CTA GTT			96
Gly Ala Tyr Gly Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val			
20	25	30	
AAA CCG ACC CAG ACC CTG ACG TTA ACC TGC ACC TTC TCC GGT TTC TCC			144
Lys Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser			
35	40	45	
CTG TCG ACC TCC GGT ATG GGT GTT TCC TGG ATC CGT CAG CCG CCG GGT			192
Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly			
50	55	60	
AAA GGT CTA GAA TGG CTG GCT CAC ATC TAC TGG GAC GAC GAC AAA CGT			240
Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg			
65	70	75	80
TAC AAC CCG AGC CTG AAA TCC CGT CTG ACG ATA TCC AAA GAC ACC TCC			288
Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser			
85	90	95	
CGT AAC CAG GTT CTG ACC ATG ACT AAC ATG GAC CCG GTT GAC ACC			336
Arg Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr			
100	105	110	
GCT ACC TAC TAC TGC GCT CGA CGC GAA ACC GTT TTC TAC TGG TAC TTC			384
Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe			
115	120	125	
GAC GTT TGG GGT CGT GGT ACC CCA GTT ACC GTG AGC TCA			423
Asp Val Trp Gly Arg Gly Thr Pro Val Thr Val Ser Ser			
130	135	140	

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser			
1	5	10	15
Gly Ala Tyr Gly Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val			
20	25	30	
Lys Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser			
35	40	45	
Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly			
50	55	60	
Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg			
65	70	75	80
Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser			
85	90	95	
Arg Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr			
100	105	110	
Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe			
115	120	125	
Asp Val Trp Gly Arg Gly Thr Pro Val Thr Val Ser Ser			
130	135	140	

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
GTC CAC TCC GAT ATC GTG ATG ACC CAG TCT CCA GAC TCG CTA GCT GTG	96
Val His Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val	
20 25 30	
TCT CTG GGC GAG AGG GCC ACC ATC AAC TGC AAG GCC TCC CAA AGT GTT	144
Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val	
35 40 45	
GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAT CAG CAG AAA CCC GGG	192
Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly	
50 55 60	
CAG CCT CCT AAG TTG CTC ATT TAC GCT GCA TCC AAT CTA GAA TCT GGG	240
Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly	
65 70 75 80	
GTA CCT GAC CGA TTC AGT GGC AGC GGG TCT GGG ACA GAT TTC ACT CTC	288
Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu	
85 90 95	
ACC ATC AGC AGC CTG CAG GCT GAA GAT GTG GCA GTA TAC TAC TGT CAG	336
Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln	

100

105

110

CAA AGT AAT GAG GAT CCT CCG AGG TTC GGC GGA GGG ACC AAG GTG GAG 384
Gln Ser Asn Glu Asp Pro Pro Arg Phe Gly Gly Thr Lys Val Glu
115 120 125

ATC AAA CGT 393
Ile Lys Arg
130

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val
20 25 30

Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val
35 40 45

Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly
65 70 75 80

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
85 90 95

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln
100 105 110

Gln Ser Asn Glu Asp Pro Pro Arg Phe Gly Gly Thr Lys Val Glu
115 120 125

Ile Lys Arg
130

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAG GCC AGC CAA AGT GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC
Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn
1 5 10 15

45

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCT GCA TCC AAT CTA GAA TCT
Ala Ala Ser Asn Leu Glu Ser
1 5

21

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala Ala Ser Asn Leu Glu Ser

1 5

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(iii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAG CAA AGT AAT GAG GAT CCT CCG ACG
Gln Gln Ser Asn Glu Asp Pro Pro Thr

1 5

27

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gln Gln Ser Asn Glu Asp Pro Pro Thr
1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACT TCT GGT ATG GGT GTG AGC
Thr Ser Gly Met Gly Val Ser
1 5

21

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Thr Ser Gly Met Gly Val Ser
1 5

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..48

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAC ATT TAC TGG GAT GAT GAC AAG CGC TAT AAC CCA TCC CTG AAG AGC	48		
His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser Leu Lys Ser			
1	5	10	15

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser Leu Lys Ser			
1	5	10	15

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGA GAG ACT GTG TTC TAC TGG TAC TTC GAT GTC
Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp Val
1 5 10

33

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CAG CAA AGT AAT GAG GAT CCT CCG AGG
Gln Gln Ser Asn Glu Asp Pro Pro Arg

1 5

27

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Gln Gln Ser Asn Glu Asp Pro Pro Arg

1 5

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTAACACTCA TTCCTGTTGA AGCTCTTGAC AATGGG

36

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTACATATGC AAGGCTTACA ACCACAATC

29

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGTTACCCCTG CGTGAATCCG GTCCGGCACT AGTTAAACCG ACCCAGACCC TGACGTTAAC 60
CTGCACCTTC TCCGGTTTCT CCCTGTCGAC CTCCGGTATG GGTGTTTCCG GGATCCG 117

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TCAGCCGCCG GGTAAAGGTC TAGAATGGCT GGCTCACATC TACTGGGACG ACGACAAACG 60
TTACAACCCG AGCCTGAAAT CCCGTCTGAC GATATCCAAA GACACCTCCC GTAACCAGGT 120

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TGTTCTGACC ATGGACCCGG TTGACACCGC TACCTACTAC TGGCGCTCGTC GCGAAACCGT 60

TTTCTACTGG TACTTCGACG TTTGGGGTCG TGGTACCCCCA GTTACCGTGA GCTCCCAACC 120

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACCCGGCGGC TGACGGATCC AGGAA 25

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATGGTCAGAA CAACCTGGTT ACGG 24

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCGGGTTAC CCTGCGTGAA TCCGG

25

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CCAACCCTCG AGTGCCATTG A

21

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CTAGCTGTGT CTCTGGCGA GAGGCCACC ATCAACTGCA AGG

43

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCTTGCAGTT GATGGTGGCC CTCTCGCCCA GAGACACAG

39

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TCGAGAGGCC TCCCAAAGTG TTGATTATGA TGGTGATAGT TATATGAACCT GGTATCAGCA

60

GAAACCC

67

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGGTTTCTGC TGATACCAGT TCATATAACT ATCACCATCA TAATCAACAC TTTGGGAGGC 60

CTC 63

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATACTACTGT CAGCAAAGTA ATGAGGGATCC TCCGAGGGTTC GGCAGGAGGGAC 51

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTGGTCCCT CCGCCGAACC TCGGAGGATC CTCATTACTT TGCTGACAGT AGT

53

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGGCAGCCTC CTAAGTTGCT CATTACGCT GCATCCAATC TAGAATCTGG GGTAC

55

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCCAGATTCT AGATTGGATG CAGCGTAAAT GAGCAACTTA GGAGGCTGCC C

51

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AATTCGAGGA CGCCAGCAAC ATGGTGTGCG AGACCCAGGT CTTCATTCT CTGTTGCTCT	60
GGATCTCTGG TGCCTACGGG CAG	83

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTAACCTGCC CGTAGGCACC AGAGATCCAG AGAACAGAG AAATGAAGAC CTGGGTCTGC	60
AACACCATGT TGCTGGCGTC CTCG	84

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CAGGTTACCC TGAAAGAGTC

20

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAAGTAGTCC TTGACCAG

18

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTCACCGTCT CCTCAGCTAG CACCAAGGGG C

31

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTTGGTGCTA GCTGAGGAGA CG

22

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CATCTAGATG GCGCCGCCAC AGTACGTTG ATCTCCAGCT TGGTCCC

47

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AAGGCCTCCC AAAGTGTGAA TTATGATGGT GATAGTTATA TGAAC

45

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACCTCCGGTA TGGGTGTTTC C

21

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CACATCTACT GGGACGACGA CAAACGTTAC AACCCGAGCC TGAAATCC

48

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CGCGAAACCG TTTTCTACTG GTACTTCGAC GTT

33

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 393 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

48

GTC CAC TCC GAT ATC GTG ATG ACC CAG TCT CCA GAC TCG CTA GCT GTG
Val His Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val
20 25 30

96

TCT CTG GGC GAG AGG GCC ACC ATC AAC TGC AAG GCC TCC CAA AGT GTT
Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val
35 40 45

144

GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAT CAG CAG AAA CCC GGG	192
Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly	
50	55
	60
CAG CCT CCT AAG TTG CTC ATT TAC GCT GCA TCC AAT CTA GAA TCT GGG	240
Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly	
65	70
	75
	80
GTA CCT GAC CGA TTC AGT GGC AGC GGG TCT GGG ACA GAT TTC ACT CTC	288
Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu	
85	90
	95
ACC ATC AGC AGC CTG CAG GCT GAA GAT GTG GCA GTA TAC TAC TGT CAG	336
Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln	
100	105
	110
CAA AGT AAT GAG GAT CCT CCG ACG TTC GGC GGA GGG ACC AAA GTG GAG	384
Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Thr Lys Val Glu	
115	120
	125
ATC AAA CGT	393
Ile Lys Arg	
130	

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1	5
	10
	15

Val His Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val
20 25 30

Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val
35 40 45

Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly
65 70 75 80

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
85 90 95

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln
100 105 110

Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu
115 120 125

Ile Lys Arg
130